

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2003, 14:59:23 ; Search time 42 seconds
(without alignments)
801.406 Million cell updates/sec

Title: US-09-745-506-37
Perfect score: 1799
Sequence: 1 MDKALLSLNDFASISPAE.....LENKINIILSETDRPLQVY 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	453.5	25.2	278 2 T40916	nggl-interacting f
2	384.5	21.4	288 2 S64243	hypothetical prote
3	285.5	15.9	373 2 A69954	conserved hypotet
4	278	15.5	366 2 F89936	conserved hypotet
5	264	14.7	268 2 G97060	uncharacterized pr
6	263.5	14.6	372 2 D83822	hypothetical prote
7	256	14.2	373 2 AH1618	conserved hypotet
8	240	13.3	373 2 AD1256	conserved hypotet
9	225	12.5	341 2 D81341	hypothetical prote
10	216.5	12.0	379 2 B70777	hypothetical prote
11	209.5	11.6	263 2 A12207	hypothetical prote
12	203.5	11.3	265 2 D95187	conserved hypotet
13	203.5	11.3	265 2 E98054	conserved hypotet
14	199.5	11.1	385 2 T44719	hypothetical prote
15	198	11.0	262 2 G82901	conserved hypotet
16	193	10.7	243 2 F71876	hypothetical prote
17	191	10.6	249 2 G64415	hypothetical prote
18	187.5	10.4	257 2 A86759	hypothetical prote
19	181	10.1	243 2 G64639	conserved hypotet
20	148	8.2	251 2 H90568	conserved hypotet
21	133	7.4	247 2 AC0588	conserved hypotet
22	129	7.2	247 2 E64806	ybg1 protein - Esc
23	129	7.2	247 2 G90720	hypothetical prote
24	129	7.2	247 2 E85571	hypothetical prote
25	117	6.5	248 2 C70158	conserved hypotet
26	112	6.2	256 2 C82119	conserved hypotet
27	109.5	6.1	316 2 E41830	RNA-directed DNA p
28	107	5.9	250 2 B71107	hypothetical prote
29	106	5.9	252 2 A83089	conserved hypotet

30	105.5	5.9	566 2 A72329	general secretion
31	102	5.7	249 2 D81954	hypothetical prote
32	100	5.6	249 2 G81011	conserved hypotet
33	98.5	5.5	1199 2 T13946	probable adaptor-r
34	98	5.4	1093 2 H84126	cation efflux syst
35	97.5	5.4	245 2 H69471	conserved hypotet
36	97.5	5.4	502 1 SKPSXR	general secretion
37	97	5.4	250 2 D75054	hypothetical prote
38	97	5.4	253 2 B84328	hypothetical prote
39	97	5.4	272 2 C75560	conserved hypotet
40	97	5.4	468 2 B64690	replicative DNA he
41	96.5	5.4	248 2 A10328	conserved hypotet
42	96.5	5.4	279 2 S64007	hypothetical prote
43	96	5.3	486 2 F71825	replicative DNA he
44	95.5	5.3	373 2 D71635	hypothetical prote
45	95	5.3	784 2 H64487	elf-4A family prob

ALIGNMENTS

```
RESULT 1
T40916
nggl-interacting factor 3 homolog - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T40916
R/Murphy, L.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, December 1998
A:Reference number: Z21956
A:Accession: T40916
A:Status: preliminary; translated from GB/EMBL/DDAJ
A:Molecule type: DNA
A:Residues: 1-278 <MDR>
A:Cross-references: EMBL:AL034490; PIDN:CAA22481.1; GSPDB:GND0068; SPDB:SPCC126.12
A:Experimental source: strain 972h-; cosmid c126
A:Genetics:
A:Gene: SPDB:SPCC126.12
A:Map position: 3
A:Introns: 72/1; 177/1; 234/1
C:Superfamily: conserved hypothetical protein YGL144c

Query Match 25.2%; Score 453.5; DB 2; Length 278;
Best Local Similarity 32.7%; Pred. No. 5.5e-29;
Matches 116; Conservative 53; Mismatches 93; Indels 93; Gaps 11;

QY 4 KALLS-----LNDPALSFAESNDVNGLVE-PSPPHYVNTLFLINDLIEEVEYLQK 57
   |||||
Db 3 KANISSKIKKVVESIVNPKLADSWDNTGLLEAFPRTNASSVLLFTDLEKVAEAIISN 62

QY 58 K-ADLISYHPPIFRPKKRTITWNTWKRLVIRALENVGIYSPTATADAPQGVNNMLAK 116
   |||||
Db 63 KLVSSIVAYHPPIIFRGKAITMEDPQDRSLKLAEGIHVYSPPTAADAADVGDNDMLAQ 122

QY 117 GLGACTSRPIHPSKAPVYPTGEGNHRVFNVTYNTDLDKVASAVGIDGVSPTSARTGN 176
   |||||
Db 123 GING-----GRNNIK-SVYPTQ----- 138

QY 177 EQQTRINLNTQKALMQVDFLSRNKQLYOKTEILLSLEKPLLHTGNGRLCTIDESVSLA 236
   |||||
Db 139 -----QNSVNAEAE-----GVRICELKIPPTLR 162

QY 237 TMDIRIKRLKLSHIRIALGVGRLESQVNVVALCAGSSGVLOGVADLYLGEMSHHD 296
   |||||
Db 163 ELVQRAKELTGLGYVOVCAPNG--LDSHISKVSLCAGSGSVVNMNDADLYFGELSHHQ 220

QY 297 TLDAASGIVVILCEHSNTERGFSLDL--BDMLDS-HLEN-KIINIILSETDRPL 347
   |||||
Db 221 VLAAAKGISVILCGHSNTERGTLKDYMCQKILASSFKEGVDAVNIYSSMDADPL 275

RESULT 2
S64243
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Db      60 TTISHHPLFEKGVTSKANGY--GLITRKLIQHDIMLIMHTMDJNPGVNNMLAKAMG 117
OY      120 ACSRRPHSPKAPNPT-----EGNHREF-----144
Db      118 LKNISITNNQDDYYVYVQYITPRDNVGPFKDLSENGLAOGEYECFESBEGRGPKPV 177
OY      145 -NWNVT-ODLDKVMASVKGIDGVSYSFSARTGNEBQTRINLCTOKALMQVDFLSRNK 202
Db      178 GEANPTIGQIDK-----IEDVDEKI-----ERMIDAYOK-----SRAE 211
OY      203 QLYOK-----TEILSEKPLLTGNGRLCTDESVSLATMIDRIKRLKLSHRLA 254
Db      212 QLKQYHPEYETPFDFEIKQTSLY--GLGVMALEVNONMTLEDFPADIKSLINIPSVRF- 268
OY      255 LGVGRFLESQVKNVALCAGS-----SSVAGVEADLYLTGEMSHHDIDMAOQGINVL 309
Db      269 --VGES--NOKIKALITGSGIGEYQAVOQG--ADVFTYGDIKRHDALDKATHGNLAD 323
OY      310 CEHSNTERGFLSDRLDMSHLE-NKINIL--SETDRDPLQVY 350
Db      324 INH-YSEYWKESLKTLLNMWFIEKINIDVEASTINTDPEFYI 366

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RESULT 5

uncharacterized protein of YbgI/Acr family [imported] - Clostridium acetobutylicum
 G97060
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: G97060
 R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: G97060
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-268 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK9274.1; PID:g15024233; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC1303

Query Match 14.7%; Score 264; DB 2; Length 268;
 Best Local Similarity 21.3%; Pred. No. 9.8e-14;
 Matches 75; Conservative 63; Mismatches 118; Indels 96; Gaps 6;

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OY      1 MDKALLSLINDFASLSFAESMDNVGLVPEPPTVNTLFLINDLTEEYMEEVLOKKAD 60
Db      3 LKKKDCNIIEDEPAPISLKEDEFNVGLMVGDRFA-SVDAIMTALDCTMDVIDAIEKNCN 61
OY      61 LLIISYPPIFRPKRTITMTWKERLYIRALENVGYSPTAYDAAPQVNNMLAKGLCA 120
Db      62 MITTHPIEFKRSKTIPTDLTKKIKIISNNINYSATNDSVKGINDAVVNLG- 120
OY      121 CTSRPHSPKAPNPTGEGNHREFVNTYQDDLDKVMASVKGIDGVSYSFSARTGNEBQT 180
Db      121 -----120
OY      181 RINLCTOKALMQVDFLSRNKQLYOKTEILSEKPLLTGNGRLCTDESVSLATMID 240
Db      121 -----FDKSSILAKNNNAVKAGIGRAVELEQNMTLKELCD 156
OY      241 RIKRHLKSHIRLALGVGRLESQVKNVALCAGSSSVLAGVE---ADLYLTGEMSHHD 297
Db      157 RVNESFKIQLSRKCGDEKKIHS---FAVINGSGODFEFEARKRGVDCITTDTSYHYV 212
OY      298 LPAASGIVNVLCEHSNTERGFLSDRLDMSHLENK-IR-TILSETDRP 346
Db      213 SDENEMNIAVIDAGHGTETPMSVYVMSKLEGLHKMGKINTPILVSONNIDP 264

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RESULT 6
 Db83822
 hypothetical protein BH1380 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: D83822
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: D83822
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-372 <STO>
 A:Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB05099.1; GSPDB:C
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH1380

Query Match 14.6%; Score 263.5; DB 2; Length 372;
 Best Local Similarity 24.9%; Pred. No. 1.8e-13;
 Matches 89; Conservative 80; Mismatches 141; Indels 47; Gaps 12;

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OY      25 VGLVPEPPTVNTLFLINDLTEEYMEEVLOKKADLLSYHPPIFRPMKRTITMTWKER 84
Db      32 IGTINRP-----IORVLTALDVMESYIDEAIEFGAELILAHNPPIFRPLSSIRTPRAYGR 86
OY      85 LVIRALENKGYSPTAYDAAPQVNNMLAKGLGACTSPRIHSPKAPNPTGEGNHREF 144
Db      87 IIRKAKHDTLTIAAHNLNDITRGVNDMAADLGLKIDVLAFT-----TTTSLKLVV 141
OY      145 NVNVTQDDLDKVMASVKGIDGVSYSFSARTGNEBQT-----RINLCTOKALMQVDF 197
Db      142 FVETHH-TDQVRRLAGAGHIGNYSYCTFNKSGTGFPEKCTNPFIOGQALEVEE 200
OY      198 L-----SRNKQLYOKTEILSEKPL-LH-----TGNGRLCTDESVSLATMI 239
Db      201 LKIEITVEGQKKVVAAMIKSHPEEPAYDVLPLANEGEFTLGIRGYLHESMTLEFA 260
OY      240 DRIKRLKSHIRLALGVGRLESQVKNVALCAGSSSVLAGV---ADLYLTGEMSHHD 296
Db      261 KQVKAFFDPTARV---VG-SLETOIRKIVAVLGGDKRYMAHALRKGAADVIVGDDYHYV 316
OY      297 TLPAASGIVNVLCEHSNTERGFLSDRLDMSHLENK--INILSETDRDPLQVY 350
Db      317 PHDALMDGLNIVPGH-NVEKIMQGYKELEKLDKKKIDTEVVASVTFDPPTFI 372

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RESULT 7

conserved hypothetical protein lln1489 [imported] - Listeria innocua (strain C11p1126
 AH1618
 C:Species: Listeria innocua
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AH1618
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entlian, K.D.; Feiht,
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maltournam, A.;
 Ok, C.; Schlueter, T.; Simoes, N.; Tlerefz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AH1618
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-373 <GLA>
 A:Cross-references: GB:AL592022; PIDN:CAC096720.1; PID:g16413962; GSPDB:GN00178
 A:Experimental source: strain C11p1126
 C:Genetics:
 A:Gene: lln1489

Query Match 14.2%; Score 256; DB 2; Length 373;
 Best Local Similarity 22.5%; Pred. No. 7.1e-13;

[illegible]

RESULT 8
AD1256
conserved hypothetical protein lmo1452 [imported] - *Listeria monocytogenes* (strain EGD-e)
C:Species: *Listeria monocytogenes*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AD1256
R:Classer, P.; Rangaoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihl, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kühn, M.; Kunst, F.; Kurapatk, G.; Madueno, E.; Maltournam, A.; Maör, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A. Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1256
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-373 <GIA>
A:Cross-references: GB:NC_003210; PIDN:CMC99530.1; PID:916410881; GSPDB:GM00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1452

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Query Match      13.3%  Score 240;  DB 2;  Length 373;
Best Local Similarity 23.7%;  Pred No.1.4e-11;
Matches      88;  Conservative      83;  Mismatches 155;  Indels      46;  Gaps      14;

QY      10  LNDFASLSPAESWMDVGLVPESPPHVNTLFLTNDLLEEWEVYLQKADLLISYHPI 69
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      13  MEKIAIPKRLAMEGDPIGLQV--GDLSRKVRKLIWFTLDVLEEVEDEAIKKVDLLIAHHP 71

QY      70  FEPMKRITMYNTEKELVITRALENRGVTSPHFAYDAAGVANNMLAKGGAQTSRPIHS 129
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      72  YAPTHIDITDQGGKKIKLIKIDITVFAAHNTLIDIAOGGVANNIADLLHONTMIIEET 131

QY      130  KAPNYPTEGNHREEVFNVTODDKVMSAV---KGIDGVSYTSESARTG--NEEOFRIN 183
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      132  YSEPRCKIAVYYPE-----NELESVRLLAVNNGAGQIQTEYECTPHHTGTGSRKPGAN 185

QY      184  LNCT--QKALQVVDFLSRNKOLYOK--TELLS-----LEKPL-LHT----- 221
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      186  AAPTIGEKALULSVSEV--KIEAIFQVYLTETITVAVKIAHDEYEGADIVVYLEMQATKE 243

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[illegible]

RESULT 9
 DB1341
 hypothetical protein Cj0705 [imported] - Campylobacter jejuni (strain NCTC 11168)
 C:Species: Campylobacter jejuni
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
 C:Accession: DB1341
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chillingworth, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Bar
 Nature 403 : 665-668, 2000
 A>Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
 A:Reference number: A61250; MUID:20150912; PMID:10688204
 A:Accession: DB1341
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-241 <PAR>
 A:Cross-references: GB:AL1139076; GB:AL111168; NID:96968128; PIDN:CA872979.1; PID:96968128
 A:Experimental source: serotype O2, strain NCTC 11168
 C:Genetics:
 A:Gene: Cj0705

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Query Match      12.5%; Score 225; DB 2; Length 241;
Best Local Similarity 19.2%; Pred. No. 1.2e-10;
Matches      68; Conservative 63; Mismatches 95; Indels 128; Gaps 9;

QY      1 MDKALSLSLNDFEASLSFSAESMDVNGVLVEFSPHTVNTLFLTNDLDEEYMEYLQKAD 60
      | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1 MKLSIYVFLDQGLSPFNQESMDNSGILLGRDSE-ISTYVLSLIDENITEKSEAN--S 57
      | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      61 LILSHPIPIFPKRIITNTWKERLYVRALENRGISPHPIYAAAGVNNMLAKIGA 120
      | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      58 LITFHPPLIFGLKDLXDYTPRAFIKEMIKYKNSLSIMHTNVDLS----- 103
      | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      121 CTSRIPIHSPKAPNYPTEGNHREFEVNVNTODLRVMSAVKGIQSVSYSESARTGNEEQT 180
      | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      104 -----HNTYPTTE-----ILGFR----- 117.

QY      181 RINLNCQKALQVVDPLSRNKQLYKTEIISLEKPLILHTGMGRCLCTIDESVSLATMID 240
      | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      118 -----ISFQDKFLIY-----VENSMSEFALCD 139

QY      241 RIKRRLKLSHTPLALGVGRITLESQYKVVVALAGSSSVLQGVADFLVTGMSHHPTIDA 300
      | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      140 WVKKRLNLIQILR---VSDCGKKDKIKRAITCGSGGDLISKVDDCFLSGDFKHOALEA 195

QY      301 ASQGINVILCEHSNTERGF---LSLDRMDLSHLENKINILISETDRDPLQV 350
      | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      196 LSNQISLIDLGHFESERFYSGCLAKDKNL-----PLQVI 230

RESULT 10
B70777
hypothetical protein Rv2230c - Mycobacterium tuberculosis (strain H37RV)
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C/Accession: B70777
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R.; Connor, R.; Davies, R.; Devlin, K.; Feltham, D.; Gentles, S.; Hamlin, N.; Holtz, R.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

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CjDate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
CjAccession: E98054
R.Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;
y, R.; LeBlanc, D.J.; Lee, L.N.; Leftkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A>Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A57872; MUID:21429245; PMID:11544234
A:Accession: E98054
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-265 <KUD>
A:Cross-references: GB:AEO07317; PIDN:AAL00266.1; PID:g15459119; GSPDB:GN00174
A:Gene: spir1462

Query Match      11.1%; Score 199.5; DB 2; Length 265;
Best Local Similarity 18.9%; Pred No. 7.3e-09;
Matches 66; Conservative 62; Mismatches 124; Indels 97; Gaps 7;

OY 6 LLSSINDPASFASMDNVGLVPEPSPTVTNTLFTNDLTVEEWEVLQKKADLLISY 65
   :: : | : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 VIQAEARCPQFESNEGSGCLQI -GTLDKGQRWVALDINEETVAEAIERGVDLIYK 64
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 66 HPPIPRPKRTITWNWKERLVRALENRGVTSPTTADAAPQVNNMLAKGLGACTSRP 125
   |||||:::~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~:
Db 65 HAPIRPRTIKDLASRPONDIVTLKHDAVVVSHTNIDIVBNGDWCQM!----- 117
   |||||:::~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~:

OY 126 IHPKAPNPTEGHNRVEENNVYTODLDKVMSAVGIDSVSTSPARSANEOTRINLN 185
   |||||:::~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~:
Db 118 -----GIETTYIQEFGPER----- 132
   |||||:::~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~:

OY 186 CTQKALMOVDFLSRNKQLYQXTEILSLKRPILLHTGMGRCLCTLDESYSLATMIRKN 245
   |||||:::~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~:
Db 133 -----GIGRICNI-QPQTFWELAQVKQV 155
   |||||:::~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~:

OY 246 LKLSHRIALGVGRLESQKVVALLACAGSGSSYLQV--EADLYTGEMSHDDTIIDAAS 302
   |||||:::~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~:
Db 156 FDLDSLRIMVHYQENDLOKFRISRVAICGGSGGFYKALKAKGADVITGDVIYTHQADMUS 215
   |||||:::~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~:

OY 303 OGGINVLCHSMTERGFLSDLRDMDSLHNK---INITLSEDRPLQ 348
   |||||:::~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~:
Db 216 DELLALDPQH-YIEVLEVEKIALLLQWKEKKGELETLLPSQASTNPF 263
   |||||:::~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~:

RESULT 14
T447719
Hypothetical protein MICB1243.36 [Imported] - Mycobacterium leprae
CjSpecies: Mycobacterium leprae
CjDate: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
CjAccession: T44719
R.Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1998
A:Reference number: Z22830
A:Accession: T44719
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-385 <PAR>
A:Cross-references: EMBL:AL023635; PIDN:CAA19217.1
A:Experimental source: cosmid B1243
CjGenetics:
A>Note: MICB1243.36

Query Match      11.1%; Score 199.5; DB 2; Length 385;
Best Local Similarity 25.5%; Pred No. 2.7e-08;
Matches 91; Conservative 59; Mismatches 170; Indels 37; Gaps 15;

OY 18 FASMDNVGLVPEPSPTVTNTLFTNDLTVEEWEVLQKKADLLSYHPPIPRPKRTIT 77
   |||||:::~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~:
Db 20 FQNSMWSVG-LVCGDEEDVELAITAVDTPRVVIDEV--PDGSLLVNHRLHLHGVDYA 76
   |||||:::~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~:

OY 78 WNTWKRRLVRALENRGVTSPTTAYDAAPQVNNMLAKGLGACTSRPTLP-----SK 130

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Db      77  VSPFQKALVRLIKSGRSFLTAHTNADSPASVDALAHVFLGVDAVLEPFLIGVASLDP 136
      131  APNF-PREGNHRV-----EFNNWTQDLDKVMSAVNGI-----DQVS-VTSPSARTGNE 177
Db      137  WVIYVPLEHVAVAQAAVEAGAGHIGDYSHCSMSVTGTGQFMPHDGSFPVSGIGALERY 196
      178  EGRFINNTQOKALMOVVDLSRNKOLYQKT-EILSLERKLLHTGGRCLTDESVSLA 236
Db      197  AEDVEVVAARAAALMSAHMAHPPEEPAFDIFALVPP-PQDVGLGRIGTLPPRESLS 255
      237  TMDIRIKRLKLSHIRIALGVGRTLESQVRY--VALCAGSGSSVYLQ-GVADL--YLtGE 291
Db      256  AFVARYGAALP---QTSSGVRATGDDMDLVSRVAVCGAGDSLSLAAVADVAQAVYTA 311
      292  MSHHDTLDAASQGINVYLCE--HSNTERGFLSDLRDLDSHLEKINIIISERDRP 346
Db      312  LRHHPA-DEHRRASNVALLIDVAHMASEFPWCGQADVLKSHFGTALSVCYCTIRTP 367

RESULT 15
conserved hypothetical U0351 [Imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence: revision 20-Aug-2000 #text: change 20-Aug-2000
C:Accession: G82901
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.R.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a
A:Reference number: A82670
A:Accession: G82901
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-262 <GL>
A:Cross-references: AF002132; GB:AF222894; NID:96899327; PIDN:AAF30760.1; GSPDB:GN
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: U0351
A:Genetic code: SGC3

Query Match      11.0%; Score 198; DB 2; Length 262;
Best Local Similarity 21.9%; Pred. No. 2e-08;
Matches 77; Conservative 59; Mismatches 104; Indels 112; Gaps 12;

      1  MDLKA-LLSSLNDPASLSFAESMDNGLVPESPPHVTNTLETLNDLIEVMEVYQAK 58
      4  MDIAQDILNFLTKKYDLSKAEMDKNGLFDEQ--QTINNVOIALDITDVAINDALINN 61
      59  ADLITSYPRPLFRPKAKRTTWTKK-RLVIRALNRRGIVSPHYAADQVNNMLAKG 117
      62  ANLITSHPRLFTNODSNDENVYFNVIDLEIKKKNKLSLTLHLAFDASANGSMQAKR 121
      118  LGACTSRPIHESKAPNPYTEGNHREFNVTQDLDKVMSAVKID-GVSYTSEFARTGN 176
      122  LGL-----LNKQEQNPYLVVGGELKLGVS----- 146
      177  EGRFINNTQOKALMOVVDLSRNKOLYQKTETLSLEKPLLLHTGGRCLTDESVSLA 236
      147  -----VDYISR---ITQKPLS---PIIKTNANFR----- 170
      237  TMDIRIKRLKLSHIRIALGVGRTLESQVRYVAACAGSG-----SSVLOGVEADLYLTGEM 292
      171  -----LENLKKIKGIIGSGYGFADDAFNRQYDMLTISDL 206
      293  SHHDTLDAASQGINVYLCEHSNTERGFLSDLRDL-----DSHLEKINII 338
      207  KYHNMIDAQAKKONIIDMNL-SSEIFLDVIYDELTKFYGDANDANLNRSLIIS 257

Search completed: August 22, 2003, 15:06:50
Job time : 44 secs

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